



Fig.1

2/11

Sequence information: *Saccharomyces cerevisiae* MFE-2 (SWISSPROT Q02207)
Length: 900 AA, Molecular weight: 98703 Da

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| | | | | | |
| MPGNLSFKDR | VVVITGAGGG | LGKVYALAYA | SRGAKVVVND | LGGTLGSGSH | NSKAADLVVD |
| 70 | 80 | 90 | 100 | 110 | 120 |
| | | | | | |
| EIKKAGGIIV | ANYDSVNENG | EKIIETAIKE | FGRVDVLINN | AGILRDVSFA | KMTEREFASV |
| 130 | 140 | 150 | 160 | 170 | 180 |
| | | | | | |
| VDVHLTGGYK | LSRAAWPYMR | SQKFGRIINT | ASPAGLFGNF | GQANYSAAKM | GLVGLAETLA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| | | | | | |
| KEGAKYNINV | NSIAPLARSR | MTENVLPPII | LKQLGPEKIV | PLVLYLTHES | TKVSNSIFEL |
| 250 | 260 | 270 | 280 | 290 | 300 |
| | | | | | |
| AAGFFGQLRW | ERSSGQIFNP | DPKTYTPEAI | LNKWEITDY | RDKPFNKTQH | PYQLSDYNDL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| | | | | | |
| ITKAKKLPPN | EQGSVKIKSL | CNKVVVVVTA | GGGLGKSHAI | WFARYGAKVV | VNDIKDPFSV |
| 370 | 380 | 390 | 400 | 410 | 420 |
| | | | | | |
| VEEINKLYGE | GTAIPDSHDV | VTEAPLIQIT | AISKFQRVDI | LVNNAGILRD | KSFLKMKDEE |
| 430 | 440 | 450 | 460 | 470 | 480 |
| | | | | | |
| WFAVLKVHLF | STFSLSKAVV | PFTKQKSGF | IINTTSTSGI | YGNFGQANYA | AAKAAILGFS |
| 490 | 500 | 510 | 520 | 530 | 540 |
| | | | | | |
| KTIALEGAKR | GIIVNVIAPH | AETAMTKTIF | SEKELSNHFD | ASQVSPLVVL | LASEELQKYS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| | | | | | |
| GRRVIGQLFE | VGGGWCQQTR | WQRSSGYVSI | KETIEPEEIK | ENWNHITDFS | RNTINPSSTE |
| 610 | 620 | 630 | 640 | 650 | 660 |
| | | | | | |
| BSSMATLQAV | QKAHSSKELD | DGLFKYTTKD | CILYNLGLGC | TSKELKYTYE | NDPDFQVLPT |
| 670 | 680 | 690 | 700 | 710 | 720 |
| | | | | | |
| FAVIPFMQAT | ATLAMDNLVD | NFNYAMLLHG | EQYFKLCTPT | MPSNGTLKTL | AKPLQVLDPN |
| 730 | 740 | 750 | 760 | 770 | 780 |
| | | | | | |
| GKAALVVGGF | ETYDIKTKKL | IAYNEGSFFI | RGAVPPEKE | VRDGKRAKFA | VQNFEVPHGK |
| 790 | 800 | 810 | 820 | 830 | 840 |
| | | | | | |
| VPDFEAEIST | NKDQAALYRL | SGDFNPLHID | PTLAKAVKFP | TPILHGLCTL | GISAKALFEH |
| 850 | 860 | 870 | 880 | 890 | 900 |
| | | | | | |
| YGPYEELKVR | FTNVVFPGDT | LKVKAWKQGS | VVVFQITDIT | RNVIVLDNAA | VKLSQAKSKL |

Fig. 2

Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A
(G to S mutation at position 16)
Length: 900 AA, Molecular weight: 98733 Da

| | | | | | |
|------------|------------|-------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MPGNLSFKDR | VVVITSAGGG | LGKVYALAYA | SRGAKVVVND | LGGTLGGSGH | NSKAADLVVD |
| 70 | 80 | 90 | 100 | 110 | 120 |
| EIKKAGGIIV | ANYDSVNENG | EKIIETAIKE | FGRVDVLINN | AGILRDVSFA | KMTEREFASV |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VDVHLTGGYK | LSRAAWPYMR | SQKFGRRIINT | ASPAGLFGNF | GQANYSAAKM | GLVGLAETLA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| KEGAKYNINV | NSIAPLARSR | MTENVLPPIH | LKQLGPEKIV | PLVLYLTHES | TKVSNSIFEL |
| 250 | 260 | 270 | 280 | 290 | 300 |
| AAGFFGQLRW | ERSSGQIFNP | DPKTYTPEAI | LNKWKETIDY | RDKPFNKTQH | PYQLSDYNDL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ITKAKKLPPN | EQGSVKIKSL | CNKVVVVVTA | GGGLGKSHAI | WFARYGAKVV | VNDIKDPFSV |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VEEINKLYGE | GTAIPDSHDV | VTEAPLIQIT | AISKFORVDI | LVNNAGILRD | KSFLKMKDEE |
| 430 | 440 | 450 | 460 | 470 | 480 |
| WFAVLKVHLF | STFSLSKAVW | PIPTKQKSGF | IINTTSTSGI | YGNFGQANYA | AKAAAILGFS |
| 490 | 500 | 510 | 520 | 530 | 540 |
| KTIALEGAKR | GIIVNVIAPI | AETAMTKTIF | SEKELSNHFD | ASQVSPVLVL | LASEELQKYS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| GRRVIGQLFE | VGGGWCQQR | WQRSSGYVSI | KETIEPEEIK | ENWNHITDFS | RNTINPSSTE |
| 610 | 620 | 630 | 640 | 650 | 660 |
| ESSMATLQAV | QKAHSSKELD | DGLFKYTTKD | CILYNLGLGC | TSKELKYTYE | NDPDFQVLPT |
| 670 | 680 | 690 | 700 | 710 | 720 |
| FAVIPFMQAT | ATLAMDNLVD | NFNYAMLLHG | EQYFKLCTPT | MPSNGTLKTL | AKPLQVLDPN |
| 730 | 740 | 750 | 760 | 770 | 780 |
| GKAALVVGGF | ETYDIKTKKL | IAYNEGSFFI | RGAVPPEKE | VRDGKRAKFA | VQNFEVPHGK |
| 790 | 800 | 810 | 820 | 830 | 840 |
| VPDFEAEIST | NKDQAALYRL | SGDFNPLHID | PTLAKAVKFP | TPILHGLCTL | GISAKALFEH |
| 850 | 860 | 870 | 880 | 890 | 900 |
| YGPYEELKVR | FTNVVFPGDT | LKVKAWKQGS | VVVFQTIDTT | RNVIVLDNAA | VKLSQAKSKL |

Fig. 3

| | | | | | |
|------------|------------|-------------|-------------|------------|-------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MPGNLSFKDR | VVVITGAGGG | LGKVYALAYA | SRGAKVVVND | LGGLTGGSGH | NSKAADLVVD |
| 70 | 80 | 90 | 100 | 110 | 120 |
| EIKKAGGIAV | ANYDSVNENG | EKIIETAIKE | FGRVDVLINN | AGILRDVSFA | KMTEREFASV |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VDVHLTGGYK | LSRAAWPYMR | SQKFGRRIINT | ASPAGLFGNF | GQANYSAAKM | GLVGLAETLA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| KEGAKYNINV | NSIAPLARSR | MTENVLPPHI | LKQLGPEKIV | PLVLYLTHES | TKVSNSIFEL |
| 250 | 260 | 270 | 280 | 290 | 300 |
| AAGFFGQLRW | ERSSGQIFNP | DPKTYTPEAI | LNKWKIEITDY | RDKPFNKTQH | PYQLSDYNDL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ITKAKKLPPN | EQGSVKIKSL | CNKVVVVVTS | GGGLGKSHAI | WFARYGAKVV | VNDIKDPFSV |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VEEINKLYGE | GTAIPDSHDV | VTEAPLIITQ | AISKFORVDI | LVNNAGILRD | KSFLKMKDEE |
| 430 | 440 | 450 | 460 | 470 | 480 |
| WFAVLKVHLF | STFSLSKAVW | PIFTKQKSGF | IINTTSTSGI | YGNFGQANYA | AAKAAILGFS |
| 490 | 500 | 510 | 520 | 530 | 540 |
| KTIALEGAKR | GIIVNVIAPH | AETAMTKTIF | SEKELSNHFD | ASQVSPLVVL | LASEELQKYS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| GRRVIGQLFE | VGGGWCQQTR | WQRSSGYVSI | KETIEPEEIK | ENWNHITDFS | RNTINPSSTE |
| 610 | 620 | 630 | 640 | 650 | 660 |
| ESSMATLQAV | QKAHSSKELD | DGLFKYTTKD | CILYNLGLGC | TSKELKYTYE | NDPDFQVLPT |
| 670 | 680 | 690 | 700 | 710 | 720 |
| FAVIPFMQAT | ATLAMDNLVD | NFNYAMLLHG | EQYFKLCTPT | MPSNGTLKTL | AKPLQVLDKN |
| 730 | 740 | 750 | 760 | 770 | 780 |
| GKAALVVGGF | ETYDIKTKKL | IAYNEGSFFI | RGAHVPPEKE | VRDGKRAKFA | VQNFEPVPHGK |
| 790 | 800 | 810 | 820 | 830 | 840 |
| VPDFEAEIST | NKDQAALYRL | SGDFNPLHID | PTLAKAVKFP | TPILHGLCTL | GISAKALFEH |
| 850 | 860 | 870 | 880 | 890 | 900 |
| YGPYEELKVR | FTNVVFPGDT | LKVKAWKOGS | VVVFOTIDTT | RNVIVLDNAA | VKLSOAKSKB |

Fig. 4

5/11

Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A+B
(G to S mutation at position 16 and position 329)
Length: 900 AA, Molecular weight: 98763 Da

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MPGNLSFKDR | VVVITSAGGG | LGKVYALAYA | SRGAKVVVND | LGGTLGGSGH | NSKAADLVVD |
| 70 | 80 | 90 | 100 | 110 | 120 |
| EIKKAGGIAV | ANYDSVNENG | EKIIETAIKE | FGRVDVLINN | AGILRDVSFA | KMTEREFASV |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VDVHLTGQYK | LSRAAWPYMR | SQKFGRIINT | ASPAGLFGNF | GQANYSAAKM | GLVGLAETLA |
| 190 | 200 | 210 | 220 | 230 | 240 |
| KEGAKYNINV | NSIAPLARSR | MTENVLPPHI | LKQLGPEKIV | PLVLYLTHES | TKVSNSIFEL |
| 250 | 260 | 270 | 280 | 290 | 300 |
| AAGFFGQLRW | ERSSGQIFNP | DPKTYTPEAI | LNKWEITDY | RDKPFNKTQH | PYQLSDYNDL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ITKAKKLPPN | EQGSVKIKSL | CNKVVVVVTS | GGGLGKSHAI | WFARYGAKVV | VNDIKDPFSV |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VEEINKLYGE | GTAIPDSHDV | VTEAPLIQIT | AISKFQRVDI | LVNNAGILRD | KSFLKMKDEE |
| 430 | 440 | 450 | 460 | 470 | 480 |
| WFAVLKVHLF | STFSLSKAVW | PIFTKQKSGF | IINTTSTSGI | YGNFGQANYA | AAKAAILGFS |
| 490 | 500 | 510 | 520 | 530 | 540 |
| KTIALEGAKR | GIIVNVIAPH | AETAMTKTIF | SEKELSNHFD | ASQVSPLVVL | LASEELQKYS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| GRRVIGQLFE | VGGGWCGQTR | WQRSSGYVSI | KETIEPEEIK | ENWNHITDFS | RNTINPSSTE |
| 610 | 620 | 630 | 640 | 650 | 660 |
| ESSMATLQAV | QKAHSSKELD | DGLFKYTTKD | CILYNLGLGC | TSKELKYTYE | NDPDFQVLPT |
| 670 | 680 | 690 | 700 | 710 | 720 |
| FAVIPFMQAT | ATLAMDNLVD | NFNyamLLHG | EQYFKLCTPT | MPSNGTLKTL | AKPLQVLDKN |
| 730 | 740 | 750 | 760 | 770 | 780 |
| GKAALVVGGF | ETYDIKTKKL | IAYNEGSFFI | RGAHVPPEKE | VRDGKRAKFA | VQNFVPHGK |
| 790 | 800 | 810 | 820 | 830 | 840 |
| VPDFEAEIST | NKDQAALYRL | SGDFNPLHID | PTLAKAVKFP | TPILHGLCTL | GISAKALFEH |
| 850 | 860 | 870 | 880 | 890 | 900 |
| YGPYEELKVR | FTNVVFPGDT | LKVKAWKQGS | VVVFQTIDTT | RNVIVLDNAA | VKLSQAKSKL |

Fig. 5

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[illegible]

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MSPVDFDKDV | VIITGAGGGL | GKYYSLEFAK | LGAKVVVNDL | GGALNGQGGN | SKAADVVVDE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| IVKNGGVAVA | DYNNVLGDGK | IVETAVKNFG | TVHVIINNAG | ILRDASMKKM | TEKDYKLVID |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VHLNGAFAVT | KAAPYFQKQ | KYGRIVNTSS | PAGLYGNFGQ | ANYASAKSAL | LGFAETLAKE |
| 190 | 200 | 210 | 220 | 230 | 240 |
| GAKYNIKANA | IAPLARSMT | ESILPPPMLE | KLGPEKVAPL | VLYLSSAENE | LTGQFFEVA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| GFYAQIRWER | SGGVLFKPDQ | SFTAEEVAKR | FSEILDYDDS | RKPEYLNQY | PFMLNDYATL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| TNEARKLPAN | DASGAPTVSL | KDKVVLITGA | GAGLGKEYAK | WFAKYGAKVV | VNDFKDATKT |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VDEIKAAGGE | AWPDQHDVAK | DSEAIKNI | DKYGTIDILV | NNAGILRDRS | FAKMSKQEW |
| 430 | 440 | 450 | 460 | 470 | 480 |
| SVQQVHLIGT | FNLSRLAWPY | FVEKQFGRII | NITSTSGIYG | NFGQANYSSS | KAGILGLSKT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| MAIEGAKNNI | KVNIVAPHA | TAMTLTIFRE | QDKNLYHADQ | VAPLLVYLGT | DDVPVTGETF |
| 550 | 560 | 570 | 580 | 590 | 600 |
| EIGGGWIGNT | RWQRAKGA | HDEHTTVEFI | KEHLNEITDF | TTDTENPKST | TESSMAILSA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| VGGDDDDDE | DREEDEGDEE | EDEEDEEEDD | PVWRFDNRDV | ILYNIALGAT | TKQLKYVYEN |
| 670 | 680 | 690 | 700 | 710 | 720 |
| DSDFQVIPTF | GHLITFNSGK | SQNSFAKLLR | NFNPMLLLHG | EHYLVKHSWP | PPTGEIKTT |
| 730 | 740 | 750 | 760 | 770 | 780 |
| FEPIATTPKG | TNVVIVHGSK | SVDNKSGLI | YSNEATYFIR | NCQADNKVYA | DRPAFATNQF |
| 790 | 800 | 810 | 820 | 830 | 840 |
| LAPKRAPDYQ | VDVPVSEDLA | ALYRLSGDRN | PLHIDPNFAK | GAKFPKPILH | GMCTYGLSAK |
| 850 | 860 | 870 | 880 | 890 | 900 |
| ALIDKFGMFN | EIKARFTGIV | FPGETLRVLA | WKESDDTIVF | QTHVVDRGTI | AINNAAIKLV |
| 906 | | | | | |
| GDKAKI | | | | | |

Fig. 6

7/11

Sequence information: *Candida tropicalis* MFE-2 mutant A
(G to S mutation in position 15)
Length: 906 AA, Molecular weight: 99499 Da

| | | | | | |
|-------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MSPVDFKDKV | VIITSAGGGL | GKYYSLEFAK | LGAKVVVNDL | GGALNGQGGN | SKAADVVVDE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| IVKNGGVAVA | DYNNVLDGDK | IVETAVKNFG | TVHVIINNAG | ILRDASMKKM | TEKDYLKVID |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VHLNGAFVAVT | KAAPYFQKQ | KYGRIVNTSS | PAGLYGNFGQ | ANYASAKSAL | LGFAETLAKE |
| 190 | 200 | 210 | 220 | 230 | 240 |
| GAKYNIKANA | IAPLARSMT | ESILPPPMLE | KLGPKEVAPL | VLYLSSAENE | LTGQFFEVA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| GFYAQIRWER | SGGVLFKPDQ | SFTAEEVAKR | FSEILDYDDS | RKPEYLNQY | PFMLNDYATL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| TNEARKLPAN | DASGAPTDSL | KDKVVLITGA | GAGLGKEYAK | WFAKYGAKVV | VNDFKDATKT |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VDEIKAAGGE | AWPDQHDVAK | DSEAIKNNVI | DKYGTIDILV | NNAGILRDRS | FAKMSKQEW |
| 430 | 440 | 450 | 460 | 470 | 480 |
| SVQQVHLIGT | FNLRLAWPY | FVEKQFGRII | NITSTSGIYG | NFGQANYSSS | KAGILGLSKT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| MAIEGAKNNI | KVNIVAPHA | TAMTLTIFRE | QDKNLYHADQ | VAPLLVYLGT | DDVPVTGETF |
| 550 | 560 | 570 | 580 | 590 | 600 |
| EIGGGWIGNT | RWQRAKAVS | HDEHTTVEFI | KEHLNEITDF | TTDTENPKST | TESSMAILSA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| VGGDDDDDE | DEEEDGDEE | EDEEDEEED | PVWRFDNRDV | ILYNIALGAT | TKQLKYVYEN |
| 670 | 680 | 690 | 700 | 710 | 720 |
| DSDFQVIPTF | GHLITFNSGK | SQNSFAKLLR | NFNPMLLLHG | EHYLVHNSWP | PPTEGEIKTT |
| 730 | 740 | 750 | 760 | 770 | 780 |
| FEPIATTPKG | TNVVIVHGSK | SVDNKGELI | YSNEATYFIR | NCQADNKVYA | DRPAFATNQF |
| 790 | 800 | 810 | 820 | 830 | 840 |
| LAPKRADPYQ | VDVPVSEDLA | ALYRLSGDRN | PLHIDPNFAK | GAKFPKPILH | GMCTYGLSAK |
| 850 | 860 | 870 | 880 | 890 | 900 |
| ALIDKFGMFN | EIKARFTGIV | FPGETLRVLA | WKESDDTIVF | QTHVVDRGTI | AINNAAIKLV |
| 906 | | | | | |
| GDKAKI | | | | | |

Fig. 7

8/11

Sequence information: *Candida tropicalis* MFE-2 mutant B
(G to S mutation in position 329)
Length: 906 AA, Molecular weight: 99499 Da

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MSPVDFKDKV | VIITGAGGGL | GKYYSLFAK | LGAKVVVNDL | GGALNGQGGN | SKAADVVVDE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| IVKNGGVAVA | DYNNVLDGDK | IVETAVKNFG | TVHVIINNAG | ILRDASMKKM | TEKDYLKVID |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VHLNGAFAVT | KAAPYFQKQ | KYGRIVNTSS | PAGLYGNFGQ | ANYASAKSAL | LGFAETLAKE |
| 190 | 200 | 210 | 220 | 230 | 240 |
| GAKYNIKANA | IAPLARSMT | ESILPPPMLE | KLGPVKVAPL | VLYLSSAENE | LTGQFFEVA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| GFYAQIRWER | SGGVLFKPDQ | SFTAEEVAKR | FSEILDYDDS | RKPEYLNQY | PFMLNDYATL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| TNEARKLPAN | DASGAPTDSL | KDKVVLITSA | GAGLGKEYAK | WFAKYGAKVV | VNDFKDATKT |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VDEIKAAGGE | AWPDQHDVAK | DSEAIKNVI | DKYGTIDILV | NNAGILRDRS | FAKMSKQEW |
| 430 | 440 | 450 | 460 | 470 | 480 |
| SVQQVHLIGT | FNLSRLAWPY | FVEKQFGRII | NITSTSGIYG | NFGQANYSSS | KAGILGLSKT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| MAIEGAKNNI | KVNIVAPHAE | TAMTLTIFRE | QDKNLYHADQ | VAPLLVYLGT | DDVPVTGETF |
| 550 | 560 | 570 | 580 | 590 | 600 |
| EIGGGWIGNT | RWQRAKGAVS | HDEHTTVEFI | KEHLNEITDF | TTDTENPKST | TESSMAILSA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| VGGDDDDDE | DEEEDGDEE | EDEEDEEDD | PVWRFDDR | ILYNIALGAT | TKQLKYVYEN |
| 670 | 680 | 690 | 700 | 710 | 720 |
| DSDFQVIPTF | GHLITFNSGK | SQNSFAKLLR | NFNPMLLLHG | EHYLVHNSWP | PPTGEIKTT |
| 730 | 740 | 750 | 760 | 770 | 780 |
| FEPIATTPKG | TNVVIVHGSK | SVDNKGELI | YSNEATYFIR | NCQADNKVYA | DRPAFATNQF |
| 790 | 800 | 810 | 820 | 830 | 840 |
| LAPKRAPDYQ | VDVPVSEDLA | ALYRLSGDRN | PLHIDPNFAK | GAKFPKPILH | GMCTYGLSAK |
| 850 | 860 | 870 | 880 | 890 | 900 |
| ALIDKFGMFN | EIKARFTGIV | FPGETLRVLA | WKESDDTIVF | QTHVVDRGTI | AINNAAIKLV |
| 906 | | | | | |
| GDKAKI | | | | | |

Fig. 8

9/11

Sequence information: *Candida tropicalis* MFE-2 mutant A+B
(G to S mutation in position 15 and position 329)
Length: 906 AA, Molecular weight: 99529 Da

| | | | | | |
|------------|------------|------------|-------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MSPVDFKDKV | VIITSAGGGL | GKYYSLEFAK | LGAKVVVNDL | GGALNGQGGN | SKAADVVVDE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| IVKNGGVAVA | DYNNVLDGDK | IVETAVKNFG | TVHVIINNAG | ILRDASMKKM | TEKDYKLVID |
| 130 | 140 | 150 | 160 | 170 | 180 |
| VHLNGAFAVT | KAAPYFQKQ | KYGRIVNTSS | PAGLYGNFGQ | ANYASAKSAL | LGFAETLAKE |
| 190 | 200 | 210 | 220 | 230 | 240 |
| GAKYNIKANA | IAPLARSMT | ESILPPPMLE | KLGPKEKVAPL | VLYLSSAENE | LTGQFFEVA |
| 250 | 260 | 270 | 280 | 290 | 300 |
| GFYAQIRWER | SGGVLFKPDQ | SFTAENVAKR | FSEILDYDDS | RKPEYLKNQY | PFMLNDYATL |
| 310 | 320 | 330 | 340 | 350 | 360 |
| TNEARKLPAN | DASGAPTDSL | KDKVVLITSA | GAGLGKEYAK | WFAKYGAKVV | VNDFKDATKT |
| 370 | 380 | 390 | 400 | 410 | 420 |
| VDEIKAAGGE | AWPDQHDVAK | DSEAIKNI | DKYGTIDILV | NNAGILRDRS | FAKMSKQEW |
| 430 | 440 | 450 | 460 | 470 | 480 |
| SVQQVHLIGT | FNLRLAWPY | FVEKQFGRII | NITSTSGIYG | NFGQANYSSS | KAGILGLSKT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| MAIEGAKNNI | KVNIVAPHA | TAMTLTIFRE | QDKNLYHADQ | VAPLLVYLGT | DDVPVTGETF |
| 550 | 560 | 570 | 580 | 590 | 600 |
| EIGGGWIGNT | RWQRAKAVS | HDEHTTVEFI | KEHLNEITDF | TTDTENPKST | TESSMAILSA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| VGGDDDDDE | DEEEDGDEE | EDEEDEEDD | PVWRFDDRDV | ILYNIALGAT | TKQLKYVYEN |
| 670 | 680 | 690 | 700 | 710 | 720 |
| DSDFQVIPTF | GHLITFNSGK | SQNSFAKLLR | NFNPMLLLHG | EHYLVHVSHP | PPTGEIKTT |
| 730 | 740 | 750 | 760 | 770 | 780 |
| FEPIATTPKG | TNVVIVHGSK | SVDNKGELI | YSNEATYFIR | NCQADNKVYA | DRPAFATNQF |
| 790 | 800 | 810 | 820 | 830 | 840 |
| LAPKRAPDYQ | VDVPVSEDLA | ALYRLSGDRN | PLHIDPNFAK | GAKFPKPILH | GMCTYGLSAK |
| 850 | 860 | 870 | 880 | 890 | 900 |
| ALIDKFGMFN | EIKARFTGIV | FPGETLRVLA | WKESDDTIVF | QTHVVDRGTI | AINNAAIKLV |
| 906 | | | | | |
| GDKAKI | | | | | |

Fig. 9

[illegible]

| | | | | | |
|--------------|------------|-------------|-------------|-------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| MGSP LRF DGR | VVLVTGAGAG | LGRAYAL AFA | ERGALVVVND | LGGDFKGVGK | GSLAADKVVE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| EIRRRGGKAV | ANYDSVEEGE | KVVKTALDAF | GRIDVVVNNA | GILRDRSFAR | ISDEDWDIIH |
| 130 | 140 | 150 | 160 | 170 | 180 |
| RVHLRGSFQV | TRAAWEHMKK | QKYGRIIMTS | SASGIYGNFG | QANYSAAKLG | LLGLANSLAI |
| 190 | 200 | 210 | 220 | 230 | 240 |
| EGRKSNIHCN | TIAPNAGSRM | TQTVMPEDLV | EALKPEYVAP | LVLWLCHESC | EENGGLFEVG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| AGWIGKLRWE | RTLGAIVRQK | NHPMTPEAVK | ANWKKICDFE | NASKPQSIQE | STGSIIEVLS |
| 310 | 320 | 330 | 340 | 350 | 360 |
| KIDSEGGVSA | NHTSRATSTA | TSGFAGAIGQ | KLPPFSYAYT | ELEAIMYALG | VGASIKDPKD |
| 370 | 380 | 390 | 400 | 410 | 420 |
| LKFIYEGSSD | FSCLPFTGVI | IGQKSMMGGG | LAEIPGLSIN | FAKVLHGEQY | LELYKPLPRA |
| 430 | 440 | 450 | 460 | 470 | 480 |
| GKLKCEAVVA | DVLDKGSGVV | IIMDVYSYSE | KELICHNQFS | LFLVGSGGFG | GKRTSDKVKV |
| 490 | 500 | 510 | 520 | 530 | 540 |
| AVAIPNRPPD | AVLTDTTSLN | QAALYRLSGD | WNPLHIDPNF | ASLAGFDKPI | LHGLCTFGFS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| ARRVLQQFAD | NDVSRFKAIK | ARFAKPVYPG | QTLQTEMWKE | GNRIHFQTKV | QETGDIVISN |
| 610 | 620 | 630 | 640 | 650 | 660 |
| AYVDLAPTSG | TSAKTPSEGG | KLQSTFVP EE | IGRRLKDIGP | EVVKKVN AVF | EWHTKGGNI |
| 670 | 680 | 690 | 700 | 710 | 720 |
| GAKWTIDLKS | GSGKVYQGPA | KGAADTTIIL | SDEDFMEVV L | GKLD PQKAFF | SGRLKARGNI |
| 730 | 736 | | | | |
| MLSQKLQMI L | KDYAKL | | | | |

Fig. 10

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Sequence information: human 17-beta-hydroxysteroid dehydrogenase 4
mutant (G to S mutation at position 16)
Length: 736 AA, Molecular weight: 79686 Da

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| | | | | | |
| MGSPLRFDGR | VVLVTSAGAG | LGRAYALAF | ERGA | LGGDFKGVGK | GSLAADKVVE |
| 70 | 80 | 90 | 100 | 110 | 120 |
| | | | | | |
| EIRRRGGKAV | ANYDSVEEGE | KVVKTALDAF | GRIDVVVNA | GILRDRSFAR | ISDEDWDIIH |
| 130 | 140 | 150 | 160 | 170 | 180 |
| | | | | | |
| RVHLRGSFQV | TRAAWEHMKK | QKYGRIIMTS | SASGIYGNFG | QANYSAAKLG | LLGLANSLAI |
| 190 | 200 | 210 | 220 | 230 | 240 |
| | | | | | |
| EGRKSNHICN | TIAPNAGSRM | TQTVMPEDLV | EALKPEYVAP | LVLWLCHESC | EENGGLFEVG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| | | | | | |
| AGWIGKLWE | RTLGAIVRQK | NHPMTPEAVK | ANWKKICDFE | NASKPQSIQE | STGSIIEVLS |
| 310 | 320 | 330 | 340 | 350 | 360 |
| | | | | | |
| KIDSEGGVSA | NHTSRATSTA | TSGFAGAIGQ | KLPPFSYAYT | ELEAIMYALG | VGASIKDPKD |
| 370 | 380 | 390 | 400 | 410 | 420 |
| | | | | | |
| LKFIYEGSSD | FSCLPTFGVI | IGQKSMGGG | LAEIPGLSIN | FAKVLHGEQY | LELYKPLPRA |
| 430 | 440 | 450 | 460 | 470 | 480 |
| | | | | | |
| GKLKCEAVVA | DVLDKGSGVV | IIMDVYSYSE | KELICHNQFS | LFLVGSGGFG | GKRTSDKVKV |
| 490 | 500 | 510 | 520 | 530 | 540 |
| | | | | | |
| AVAIPNRPPD | AVLTDTTSLN | QAALYRLSGD | WNPLHIDPNF | ASLAGFDKPI | LHGLCTFGFS |
| 550 | 560 | 570 | 580 | 590 | 600 |
| | | | | | |
| ARRVLQQFAD | NDVSRFKAIK | ARFAKPVYPG | QTLQTEMWKE | GNRIHFQTKV | QETGDIVISN |
| 610 | 620 | 630 | 640 | 650 | 660 |
| | | | | | |
| AYVDLAPTSG | TSAKTPSEGG | KLQSTFVFEE | IGRRLKDIGP | EVVKVNAVAF | EWHTKGGNI |
| 670 | 680 | 690 | 700 | 710 | 720 |
| | | | | | |
| GAKWTIDLKS | GSGKVYQGPA | KGAADTTIIL | SDEDFMEVVL | GKLDPQKAFF | SGRLKARGNI |
| 730 | 736 | | | | |
| | | | | | |
| MLSQKLQMIL | KDYAKL | | | | |

Fig. 11

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